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Amendments to the Specification:

Please amend the paragraph beginning on page 10, line 21, as follows:

-- Homologous amino acid or nucleotide sequences preferably comprise enough of the amino acid sequence of a polypeptide or the nucleotide sequence of a gene to afford putative identification of that polypeptide or gene, either by manual evaluation of the sequence by one skilled in the art, or by computer-automated sequence comparison and identification using algorithms such as BLAST (Basic Local Alignment Search Tool) (for a review see Altschul, et al., Meth Enzymol. 266:460, 1996; and Altschul, et al., Nature Genet. 6:119, 1994). BLAST is the heuristic search algorithm employed by the programs blastp, blastn, blastx, tblastn, and tblastx using the statistical methods of Karlin and Altschul (~~Internet~~available on the world wide web at site:www.ncbi.nih.gov/BLAST/; Altschul, et al., J. Mol. Biol. 215:403, 1990). The BLAST programs were tailored for sequence similarity searching, for example to identify homologues to a query sequence. The BLAST pages offer several different databases for searching. Some of these, like ecoli, dbEST and month, are subsets of the NCBI (National Center for Biotechnology Information) databases. Others, such as SwissProt, PDB and Kabat are compiled outside of NCBI. Protein BLAST allows one to input protein sequences and compare these against other protein sequences. --

Please amend the paragraph beginning on page 11, line 7, as follows:

-- The five BLAST programs available ~~at Internet~~ on the world wide web at site:www.ncbi.nlm.nih.gov perform the following tasks: --

Please amend the paragraph beginning on page 36, line 6, as follows:

-- BLAST (Basic Local Alignment Search Tool) is a computer-automated amino acid sequence and nucleic acid sequence comparison and identification tool. The heuristic search algorithm BLAST 2.2.1 (Altschul, et al., Nucleic Acids Res. 25:3389, 1997; Altschul, et al., J. Mol. Biol. 215:403, 1990; and Madden, et al., Meth. Enzymol. 266:131, 1996, incorporated herein by reference) was used to search for proteins similar to the BZRI protein sequence. The BLASTP tool (available on

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the world wide web at ~~www~~.ncbi.nih.gov/BLAST) takes protein sequences in FASTA format, GenBank Accession numbers or GI numbers and compares them against the NCBI protein databases.) The BZR1 sequence was queried against the non-redundant database using the standard protein-protein BLASTP version 2.2.1 (Apr. 13, 2001) with the following settings: matrix=BLOSUM62, gap costs: Existence: 11, Extension: 1. The % identity and % similarity (positives) measurements were determined by a pairwise blast search "BLAST 2 sequences" results version BLASTP"(Tatusova, et al., FEMS Microbiol Lett. 174:247, 1999, incorporated herein by reference) --

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